

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Micromet GmbH
 (B) STREET: Am Klopferspitz 19
 (C) CITY: Martinsried
 (D) STATE: none
 (E) COUNTRY: Germany
 (F) POSTAL CODE (ZIP): 82152

(ii) TITLE OF INVENTION: Novel antibodies and human dendritic cell population and uses thereof

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAG	GTC	CAA	CTG	CAG	CAG	TCA	GGG	GCT	GAG	CTT	GTG	AAG	CCT	GGG	GCT	48
Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	
1				5					10					15		
TCA	GTG	AAG	CTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	CTC	ACC	AGC	TAC	96
Ser	Val	Lys	Leu	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Leu	Thr	Ser	Tyr	
			20					25					30			
TGG	TTG	CAC	TGG	GTG	AAG	CAG	TGG	CCT	GGA	CGA	GGC	CTT	GAG	TGG	ATT	144
Trp	Leu	His	Trp	Val	Lys	Gln	Trp	Pro	Gly	Arg	Gly	Leu	Glu	Trp	Ile	
		35					40						45			

GGA AGG ATT GAT CCC AAT AGT GGT GGT ACT AAG TAC GAT GAG AAG TTC	192
Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Tyr Asp Glu Lys Phe	
50 55 60	
AAG AGC AAG GCC ACA CTG ACT GTA GAC AAA CCC TCC AGC ACA GCC TAC	240
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr	
65 70 75 80	
ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAT TGT	288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
GCA AGA TGG GAC TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA	336
Ala Arg Trp Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala	
1 5 10 15	
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr	
20 25 30	
Trp Leu His Trp Val Lys Gln Trp Pro Gly Arg Gly Leu Glu Trp Ile	
35 40 45	
Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Tyr Asp Glu Lys Phe	
50 55 60	
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr	
65 70 75 80	
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg Trp Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
100 105 110	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAC ATT CAG CTG ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG	48
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly	
115 120 125	
GAA AAG GTC ACC ATG ACC TGC AGG GCC AGC TCA AGT GTT AGT TCC AGT	96
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser	
130 135 140	
TAC TTG CAC TGG TAC CAG CAG AAG TCA GGT GCC TCC CCC AAA CTC TGG	144
Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp	
145 150 155 160	
ATT TAT AGC ACA TCC AAC TTG GCT TCT GGA GTC CCT GCT CGC TTC AGT	192
Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser	
165 170 175	
GGC AGT GGG TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC AGT GTG GAG	240
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu	
180 185 190	
GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TAC AGT GGT TAC CCG	288
Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro	
195 200 205	
TAC ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC AAA	324
Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
210 215 220	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly	
1 5 10 15	
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser	
20 25 30	

Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp
 35 40 45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu
 65 70 75 80

Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro
 85 90 95

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

RECEIVED
 JUL 10 1964
 U.S. DEPT. OF AGRICULTURE
 WASHINGTON, D.C.

SEQUENCE LISTING

<110> MICROMET GMBH

<120> Novel antibodies and human dendritic cell population and uses thereof

<130> B 3357 PCT

<140>

<141>

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 336

<212> DNA

<213> Homo sapiens

<400> 1

```
cagggtccaac tgcagcagtc aggggctgag cttgtgaagc ctggggcttc agtgaagctg 60
tcttgcaagg cttctggcta caccctcacc agctactggg tgcactgggt gaagcagtgg 120
cctggacgag gccttgagtg gattggaagg attgatccca atagtgggtg tactaagtac 180
gatgagaagt tcaagagcaa ggccacactg actgtagaca aaccctccag cacagcctac 240
atgcagctca gcagcctgac atctgaggac tctgcggtct attattgtgc aagatggggac 300
tactgggggcc aagggaccac ggtcaccgtc tcttca 336
```

<210> 2

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2

```
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Leu Thr Ser Tyr
20 25 30
Trp Leu His Trp Val Lys Gln Trp Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45
Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Tyr Asp Glu Lys Phe
50 55 60
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Trp Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110
```

<210> 3

<211> 324
 <212> DNA
 <213> Homo sapiens

<400> 3
 gacattcagc tgaccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 60
 atgacctgca gggccagctc aagtgttagt tccagttact tgcactggta ccagcagaag 120
 tcagggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtcctt 180
 gctcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagtgtggag 240
 gctgaagatg ctgccactta ttactgccag cagtacagtg gttaccgta cacgttcgga 300
 ggggggacca agctggagat caaa 324

<210> 4
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 4
 Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15
 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp
 35 40 45
 Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu
 65 70 75 80
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Gly Tyr Pro
 85 90 95
 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105